

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/444,762

DATE: 12/13/1999
TIME: 23:45:23

INPUT SET: S34198.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

1
2
3 (1) General Information
4
5 (i) APPLICANT: Bryan, Bruce
6
7 (ii) TITLE OF INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
8
9 (iii) NUMBER OF SEQUENCES: 14
10
11 (iv) CORRESPONDENCE ADDRESS:
12 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
13 (B) STREET: 4250 Executive Square, 7th Floor
14 (C) CITY: La Jolla
15 (D) STATE: CA
16 (E) COUNTRY: USA
17 (F) ZIP: 92037
18
19 (v) COMPUTER READABLE FORM:
20 (A) MEDIUM TYPE: Diskette
21 (B) COMPUTER: IBM Compatible
22 (C) OPERATING SYSTEM: DOS
23 (D) SOFTWARE: FastSEQ Version 1.5
24
25 (vi) CURRENT APPLICATION DATA:
26 (A) APPLICATION NUMBER:
27 (B) FILING DATE:
28 (C) CLASSIFICATION:
29
30 (vii) PRIOR APPLICATION DATA:
31 (A) APPLICATION NUMBER: 0909/135,988
32 (B) FILING DATE: 08-17-98
33 (C) CLASSIFICATION:
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: 08/757,046
37 (B) FILING DATE: 11-25-96
38 (C) CLASSIFICATION:
39
40 (vii) PRIOR APPLICATION DATA:
41 (A) APPLICATION NUMBER: 08/597,274
42 (B) FILING DATE: 02-06-96
43
44 (viii) ATTORNEY/AGENT INFORMATION:
45 (A) NAME: Seidman, Stephanie L
46 (B) REGISTRATION NUMBER: 33,779

RAW SEQUENCE LISTING
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47 (C) REFERENCE/DOCKET NUMBER: 24727-105C
48
49 (ix) TELECOMMUNICATION INFORMATION:
50 (A) TELEPHONE: 619-450-8400
51 (B) TELEFAX: 619-450-8499
52 (C) TELEX:
53
54 (2) INFORMATION FOR SEQ ID NO:1:
55
56 (i) SEQUENCE CHARACTERISTICS:
57 (A) LENGTH: 1196 base pairs
58 (B) TYPE: nucleic acid
59 (C) STRANDEDNESS: single
60 (D) TOPOLOGY: linear
61
62 (ii) MOLECULE TYPE: cDNA
63
64 (vi) ORIGINAL SOURCE:
65
66 (ix) FEATURE:
67
68 (A) NAME/KEY: Coding Sequence
69 (B) LOCATION: 1...942
70 (D) OTHER INFORMATION: Renilla Reinformis Luciferase
71
72 (x) PUBLICATION INFORMATION:
73
74 PATENT NO.: 5,418,155
75
76 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
77
78 AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG 48
79 Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
80 1 5 10 15
81
82 ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT 96
83 Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
84 20 25 30
85
86 CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT 144
87 Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
88 35 40 45
89
90 GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA 192
91 Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
92 50 55 60
93
94 CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT 240
95 His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
96 65 70 75 80
97
98 CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG 288
99 Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg

RAW SEQUENCE LISTING PATENT APPLICATION US/09/444,762

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TIME: 23:45:23

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	85	90	95	
100				
101				
102	TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT			336
103	Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile			
104	100	105	110	
105				
106	TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG			384
107	Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu			
108	115	120	125	
109				
110	GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT			432
111	Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val			
112	130	135	140	
113				
114	CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT			480
115	His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro			
116	145	150	155	160
117				
118	GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA			528
119	Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys			
120	165	170	175	
121				
122	ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA			576
123	Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys			
124	180	185	190	
125				
126	ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA			624
127	Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro			
128	195	200	205	
129				
130	TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT			672
131	Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg			
132	210	215	220	
133				
134	GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT			720
135	Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val			
136	225	230	235	240
137				
138	AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG			768
139	Arg Asn Tyr Asn Ala Tyr Leu Arg Ala Ser Asp Asp Leu Pro Lys Met			
140	245	250	255	
141				
142	TTT ATT GAA TCG GAT CCA GGA TTC TTT TCC AAT GCT ATT GTT GAA GGC			816
143	Phe Ile Glu Ser Asp Pro Gly Phe Phe Ser Asn Ala Ile Val Glu Gly			
144	260	265	270	
145				
146	GCC AAG AAG TTT CCT AAT ACT GAA TTT GTC AAA GTA AAA GGT CTT CAT			864
147	Ala Lys Lys Phe Pro Asn Thr Glu Phe Val Lys Val Lys Gly Leu His			
148	275	280	285	
149				
150	TTT TCG CAA GAA GAT GCA CCT GAT GAA ATG GGA AAA TAT ATC AAA TCG			912
151	Phe Ser Gln Glu Asp Ala Pro Asp Glu Met Gly Lys Tyr Ile Lys Ser			
152	290	295	300	

RAW SEQUENCE LISTING PATENT APPLICATION US/09/444,762

DATE: 12/13/1999
TIME: 23:45:24

INPUT SET: S34198.raw

153
154 TTC GTT GAG CGA GTT CTC AAA AAT GAA CAA TAA TTACTTTGGT TTTTATTTA 965
155 Phe Val Glu Arg Val Leu Lys Asn Glu Gln
156 305 310
157
158 CATTTTTCCTT GGGTTTAATA ATATAAATGT CATTTTCAAC AATTTTATTT TAACTGAATA 1025
159 TTTCACAGGG AACATTCATA TATGTTGATT AATTTAGCTC GAACTTTACT CTGTCATATC 1085
160 ATTTTGAAT ATTACCTCTT TCAATGAAAC TTTATAAACA GTGGTTCAAT TAATTAATAT 1145
161 ATATTATAAT TACATTTGTT ATGTAATAAA CTCGGTTTTA TTATAAAAAA A 1196
162

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...1665
- (D) OTHER INFORMATION: Cypridina hilgendorffii luciferase

(x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

184
185 ATG AAG CTA ATA ATT CTG TCT ATT ATA TTG GCC TAC TGT GTC ACA GTC 48
186 Met Lys Leu Ile Ile Leu Ser Ile Ile Leu Ala Tyr Cys Val Thr Val
187 1 5 10 15
188
189 AAC TGC CAG GAT GCA TGT CCT GTA GAA GCT GAA GCA CCG TCA AGT ACA 96
190 Asn Cys Gln Asp Ala Cys Pro Val Glu Ala Glu Ala Pro Ser Ser Thr
191 20 25 30
192
193 CCA ACA GTC CCA ACA TCT TGT GAA GCT AAA GAA GGA GAA TGT ATC GAT 144
194 Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp
195 35 40 45
196
197 ACC AGA TGC GCA ACA TGT AAA CGA GAC ATA CTA TCA GAC GGA CTG TGT 192
198 Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys
199 50 55 60
200
201 GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTA ATT 240
202 Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile
203 65 70 75 80
204
205 GAA TCC AGA GTA GAA GCT GCT GGA TAT TTT AGA ACG TTT TAC GCC AAA 288

RAW SEQUENCE LISTING PATENT APPLICATION US/09/444,762

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206	Glu Ser Arg Val Glu Ala Ala Gly Tyr Phe Arg Thr Phe Tyr Ala Lys	
207	85 90 95	
208		
209	AGA TTT AAT TTT CAG GAA CCT GGT AAA TAT GTG CTG GCT CGA GGA ACC	336
210	Arg Phe Asn Phe Gln Glu Pro Gly Lys Tyr Val Leu Ala Arg Gly Thr	
211	100 105 110	
212		
213	AAG GGT GGC GAC TGG TCT GTA ACC CTC ACC ATG GAG AAT CTA GAT GGA	384
214	Lys Gly Gly Asp Trp Ser Val Thr Leu Thr Met Glu Asn Leu Asp Gly	
215	115 120 125	
216		
217	CAG AAG GGA GCT GTA CTG ACT AAG ACA ACA CTG GAG GTA GTA GGA GAC	432
218	Gln Lys Gly Ala Val Leu Thr Lys Thr Thr Leu Glu Val Val Gly Asp	
219	130 135 140	
220		
221	GTA ATA GAC ATT ACT CAA GCT ACT GCA GAT CCT ATC ACA GTT AAC GGA	480
222	Val Ile Asp Ile Thr Gln Ala Thr Ala Asp Pro Ile Thr Val Asn Gly	
223	145 150 155 160	
224		
225	GGA GCT GAC CCA GTT ATC GCT AAC CCG TTC ACA ATT GGT GAG GTG ACC	528
226	Gly Ala Asp Pro Val Ile Ala Asn Pro Phe Thr Ile Gly Glu Val Thr	
227	165 170 175	
228		
229	ATT GCT GTT GTC GAA ATA CCC GGC TTC AAT ATT ACA GTC ATC GAA TTC	576
230	Ile Ala Val Val Glu Ile Pro Gly Phe Asn Ile Thr Val Ile Glu Phe	
231	180 185 190	
232		
233	TTT AAA CTA ATC GTG ATA GAT ATT CTG GGA GGA AGA TCT GTG AGA ATT	624
234	Phe Lys Leu Ile Val Ile Asp Ile Leu Gly Gly Arg Ser Val Arg Ile	
235	195 200 205	
236		
237	GCT CCA GAC ACA GCA AAC AAA GGA CTG ATA TCT GGT ATC TGT GGT AAT	672
238	Ala Pro Asp Thr Ala Asn Lys Gly Leu Ile Ser Gly Ile Cys Gly Asn	
239	210 215 220	
240		
241	CTG GAG ATG AAT GAC GCT GAT GAC TTT ACT ACA GAC GCA GAT CAG CTG	720
242	Leu Glu Met Asn Asp Ala Asp Asp Phe Thr Thr Asp Ala Asp Gln Leu	
243	225 230 235 240	
244		
245	GCG ATC CAA CCC AAC ATA AAC AAA GAG TTC GAC GGC TGC CCA TTC TAC	768
246	Ala Ile Gln Pro Asn Ile Asn Lys Glu Phe Asp Gly Cys Pro Phe Tyr	
247	245 250 255	
248		
249	GGG AAT CCT TCT GAT ATC GAA TAC TGC AAA GGT CTC ATG GAG CCA TAC	816
250	Gly Asn Pro Ser Asp Ile Glu Tyr Cys Lys Gly Leu Met Glu Pro Tyr	
251	260 265 270	
252		
253	AGA GCT GTA TGT CGT AAC AAT ATC AAC TTC TAC TAT TAC ACT CTG TCC	864
254	Arg Ala Val Cys Arg Asn Asn Ile Asn Phe Tyr Tyr Tyr Thr Leu Ser	
255	275 280 285	
256		
257	TGC GCC TTC GCT TAC TGT ATG GGA GGA GAA GAA AGA GCT AAA CAC GTC	912
258	Cys Ala Phe Ala Tyr Cys Met Gly Gly Glu Glu Arg Ala Lys His Val	

PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/444,762

DATE: 12/13/1999
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INPUT SET: S34198.raw

Line

Error

Original Text